

<110> Dartois, Veronique A.
Hoch, James A.
Valle, Fernando
Kumar, Manoj

att acg gaa gat tta ggc att acc aaa ggc atc tcg tcg ctt ctt ggc 258
Ile Thr Glu Asp Leu Gly Ile Thr Lys Gly Ile Ser Ser Leu Leu Gly
40 45 50 55

gca ctt ttc ttc ctc ggc tat ttc ttc ttc cag atc ccg ggg gcg att	306
Ala Leu Phe Phe Leu Gly Tyr Phe Phe Phe Gln Ile Pro Gly Ala Ile	
60 65 70	
tac gcg gaa cgc cgt agc gta cgg aag ctg att ttc atc tgt ctg atc	354
Tyr Ala Glu Arg Arg Ser Val Arg Lys Leu Ile Phe Ile Cys Leu Ile	
75 80 85	
ctg tgg ggc gcc tgc gcc tcg ctt gac cgg gat ggt gca caa tat tcc	402
Leu Trp Gly Ala Cys Ala Ser Leu Asp Arg Asp Gly Ala Gln Tyr Ser	
90 95 100	
agc gct ggc tgg cga tcc gtt tta ttc tcg gct gtc gtg gaa gcg gcg	450
Ser Ala Gly Trp Arg Ser Val Leu Phe Ser Ala Val Val Glu Ala Ala	
105 110 115	
gtc atg ccg gcg atg ctg att tac atc agt aac tgg ttt acc aaa tca	498
Val Met Pro Ala Met Leu Ile Tyr Ile Ser Asn Trp Phe Thr Lys Ser	
120 125 130 135	
gaa cgt tca cgc gcc aac acc ttc tta atc ctc ggc aac ccg gtc acg	546
Glu Arg Ser Arg Ala Asn Thr Phe Leu Ile Leu Gly Asn Pro Val Thr	
140 145 150	
gta ctg tgg atg tcg gtg gtc tcc ggc tac ctg att cag tcc ttc ggc	594
Val Leu Trp Met Ser Val Val Ser Gly Tyr Leu Ile Gln Ser Phe Gly	
155 160 165	
tgg cgt gaa atg ttt att att gaa ggc gtt ccg gcc gtc ctc tgg gcc	642
Trp Arg Glu Met Phe Ile Ile Glu Gly Val Pro Ala Val Leu Trp Ala	
170 175 180	
ttc tgc tgg tgg gtg ctg gtc aaa gtt aaa ccg tcg cag gtg aac tgg	690
Phe Cys Trp Trp Val Leu Val Lys Val Lys Pro Ser Gln Val Asn Trp	
185 190 195	
ttg tcg gaa aac gag aaa gcc gcg ctg cag gcg cag ctg gag agc gag	738
Leu Ser Glu Asn Glu Lys Ala Ala Leu Gln Ala Gln Leu Glu Ser Glu	
200 205 210 215	
cag cag ggt att aaa gcc gtg cgt aac tac ggc gaa gcc ttc cgc tca	786
Gln Gln Gly Ile Lys Ala Val Arg Asn Tyr Gly Glu Ala Phe Arg Ser	
220 225 230	
cgc aac gtc att cta ctg tgc atg cag tat ttt gcc tgg agt atc ggc	834
Arg Asn Val Ile Leu Leu Cys Met Gln Tyr Phe Ala Trp Ser Ile Gly	
235 240 245	
gtg tac ggt ttt gtg ctg tgg ttg ccg tca att att cgc agc ggc ggc	882
Val Tyr Gly Phe Val Leu Trp Leu Pro Ser Ile Ile Arg Ser Gly Gly	
250 255 260	

005030-005030

gtc aat atg ggg atg gtg gaa gtc ggc tgg ctc tct tgc gtg cct tat	930
Val Asn Met Gly Met Val Glu Val Gly Trp Leu Ser Ser Val Pro Tyr	
265 270 275	
ctg gcc gcg act att gcg atg atc gtc gtc tcc tgg gct tcc gat aaa	978
Leu Ala Ala Thr Ile Ala Met Ile Val Val Ser Trp Ala Ser Asp Lys	
280 285 290 295	
atg cag aac cgt aaa ctg ttc gtc tgg ccg ctg ctg ctg att ggc gga	1026
Met Gln Asn Arg Lys Leu Phe Val Trp Pro Leu Leu Leu Ile Gly Gly	
300 305 310	
ctg gct ttt att ggc tca tgg gcc gtc ggc gct aac cat ttc tgg gcc	1074
Leu Ala Phe Ile Gly Ser Trp Ala Val Gly Ala Asn His Phe Trp Ala	
315 320 325	
tct tat acc ctg ctg gtg att gcc aat gcg gca atg tac gcc cct tac	1122
Ser Tyr Thr Leu Leu Val Ile Ala Asn Ala Ala Met Tyr Ala Pro Tyr	
330 335 340	
ggc ccg ttt ttc gcc atc att ccg gaa atg ctg ccg cgt aac gtc gcc	1170
Gly Pro Phe Phe Ala Ile Ile Pro Glu Met Leu Pro Arg Asn Val Ala	
345 350 355	
ggc gcc gca atg gcg ctc atc aac agc atg ggg gcc tta ggt tca ttc	1218
Gly Gly Ala Met Ala Leu Ile Asn Ser Met Gly Ala Leu Gly Ser Phe	
360 365 370 375	
ttt ggt tgc tgg ttc gtg gcc tac ctg aac gcc acc acc gcc agt cca	1266
Phe Gly Ser Trp Phe Val Gly Tyr Leu Asn Gly Thr Thr Gly Ser Pro	
380 385 390	
tca gcc tca tac att ttc atg gga gtg gcg ctt ttc gcc tgc gta tgg	1314
Ser Ala Ser Tyr Ile Phe Met Gly Val Ala Leu Phe Ala Ser Val Trp	
395 400 405	
ctt act tta att gtt aag cct gct aac aat caa aag ctc ccc atc ggc	1362
Leu Thr Leu Ile Val Lys Pro Ala Asn Asn Gln Lys Leu Pro Ile Gly	
410 415 420	
gct cgt cac gcc tgacctttac tacttacgga gatcacgcct tgggtacgtt	1414
Ala Arg His Ala	
425	
gcaggacaaa ccgataggca ccgcaaaggc tggggccatc gagcagcgcg taaacagtca	1474
gctgggttgct gtcgctgtgc ggcgtc	1500

<210> 2

<211> 427

<212> PRT

<213> Unknown

<220>

FOE080-10522660

<400> 2

Met 1	Asn	Ser	Ser	Thr 5	Asn	Ala	Thr	Lys	Arg 10	Trp	Trp	Tyr	Ile	Met 15	Pro
Ile	Val	Phe	Ile	Thr	Tyr	Ser	Leu	Ala	Tyr	Leu	Asp	Arg	Ala	Asn	Phe
			20					25					30		
Ser	Phe	Ala	Ser	Ala	Ala	Gly	Ile	Thr	Glu	Asp	Leu	Gly	Ile	Thr	Lys
		35					40					45			
Gly	Ile	Ser	Ser	Leu	Leu	Gly	Ala	Leu	Phe	Phe	Leu	Gly	Tyr	Phe	Phe
	50					55					60				
Phe	Gln	Ile	Pro	Gly	Ala	Ile	Tyr	Ala	Glu	Arg	Arg	Ser	Val	Arg	Lys
65				70						75				80	
Leu	Ile	Phe	Ile	Cys	Leu	Ile	Leu	Trp	Gly	Ala	Cys	Ala	Ser	Leu	Asp
			85					90					95		
Arg	Asp	Gly	Ala	Gln	Tyr	Ser	Ser	Ala	Gly	Trp	Arg	Ser	Val	Leu	Phe
			100					105					110		
Ser	Ala	Val	Val	Glu	Ala	Ala	Val	Met	Pro	Ala	Met	Leu	Ile	Tyr	Ile
		115					120					125			
Ser	Asn	Trp	Phe	Thr	Lys	Ser	Glu	Arg	Ser	Arg	Ala	Asn	Thr	Phe	Leu
	130					135					140				
Ile	Leu	Gly	Asn	Pro	Val	Thr	Val	Leu	Trp	Met	Ser	Val	Val	Ser	Gly
145				150						155				160	
Tyr	Leu	Ile	Gln	Ser	Phe	Gly	Trp	Arg	Glu	Met	Phe	Ile	Ile	Glu	Gly
			165					170						175	
Val	Pro	Ala	Val	Leu	Trp	Ala	Phe	Cys	Trp	Trp	Val	Leu	Val	Lys	Val
			180					185					190		
Lys	Pro	Ser	Gln	Val	Asn	Trp	Leu	Ser	Glu	Asn	Glu	Lys	Ala	Ala	Leu
		195					200					205			
Gln	Ala	Gln	Leu	Glu	Ser	Glu	Gln	Gln	Gly	Ile	Lys	Ala	Val	Arg	Asn
	210					215					220				
Tyr	Gly	Glu	Ala	Phe	Arg	Ser	Arg	Asn	Val	Ile	Leu	Leu	Cys	Met	Gln
225				230						235				240	
Tyr	Phe	Ala	Trp	Ser	Ile	Gly	Val	Tyr	Gly	Phe	Val	Leu	Trp	Leu	Pro
			245					250						255	
Ser	Ile	Ile	Arg	Ser	Gly	Gly	Val	Asn	Met	Gly	Met	Val	Glu	Val	Gly
			260					265					270		
Trp	Leu	Ser	Ser	Val	Pro	Tyr	Leu	Ala	Ala	Thr	Ile	Ala	Met	Ile	Val
		275					280					285			
Val	Ser	Trp	Ala	Ser	Asp	Lys	Met	Gln	Asn	Arg	Lys	Leu	Phe	Val	Trp
	290					295					300				
Pro	Leu	Leu	Leu	Ile	Gly	Gly	Leu	Ala	Phe	Ile	Gly	Ser	Trp	Ala	Val
305				310						315				320	
Gly	Ala	Asn	His	Phe	Trp	Ala	Ser	Tyr	Thr	Leu	Leu	Val	Ile	Ala	Asn
			325					330						335	
Ala	Ala	Met	Tyr	Ala	Pro	Tyr	Gly	Pro	Phe	Phe	Ala	Ile	Ile	Pro	Glu
			340					345					350		
Met	Leu	Pro	Arg	Asn	Val	Ala	Gly	Gly	Ala	Met	Ala	Leu	Ile		

Ala Leu Phe Ala Ser Val Trp Leu Thr Leu Ile Val Lys Pro Ala Asn
 405 410 415
 Asn Gln Lys Leu Pro Ile Gly Ala Arg His Ala
 420 425

<210> 3
 <211> 1775
 <212> DNA
 <213> Unknown

<220>
 <223> environmental source

<221> CDS
 <222> (214)...(1491)

<400> 3
 ggcaatttgc ggtgtttttt ccgcaggacg ttcacgtgcc ggccgtgtatt catcaacggc 60
 cctgcgctat tcgcaaagtg gtggtgaaaa taccgctgcg ttatttaacg cccaataagc 120
 aacaccgagt ttataaccct gaacgacacg gctgcgggcc tgtgtagacg cccctacgcc 180
 ttaacaccac taaatgactc tacaggtgta tat atg aat aca gcc tct gtt tct 234
 Met Asn Thr Ala Ser Val Ser
 1 5

gtc acc caa agc cag gcg atc ccc aaa tta cgc tgg ttg aga ata gtg 282
 Val Thr Gln Ser Gln Ala Ile Pro Lys Leu Arg Trp Leu Arg Ile Val
 10 15 20

cgc cct att ctt att acc tgc att att tcc tat atg gac cgg gtg aac 330
 Pro Pro Ile Leu Ile Thr Cys Ile Ile Ser Tyr Met Asp Arg Val Asn
 25 30 35

atc gcc ttc gcc atg ccc ggc ggc atg gac gat gaa ctg ggc atc acc 378
 Ile Ala Phe Ala Met Pro Gly Gly Met Asp Asp Glu Leu Gly Ile Thr
 40 45 50 55

gcc tcg atg gcc ggg ttg gcc ggc ggt att ttc ttt atc ggt tat ctg 426
 Ala Ser Met Ala Gly Leu Ala Gly Gly Ile Phe Phe Ile Gly Tyr Leu
 60 65 70

ttc ttg cag gta ccc ggc ggc aag ctg gcg gtg tac ggc aac ggc aag 474
 Phe Leu Gln Val Pro Gly Gly Lys Leu Ala Val Tyr Gly Asn Gly Lys
 75 80 85

aaa ttc atc ggt tgg tcg ttg ttg gcc tgg gcg gtg att tcc gtg ctg 522
 Lys Phe Ile Gly Trp Ser Leu Leu Ala Trp Ala Val Ile Ser Val Leu
 90 95 100

acc ggg ctg gtc acg aat cag tat caa ttg ctg ttc ctg cgc ttc gcc 570
 Thr Gly Leu Val Thr Asn Gln Tyr Gln Leu Leu Phe Leu Arg Phe Ala
 105 110 115

09922501.080304

ctc ggc cgt ttc cga agc ggc atg ctg cgg tgg gtg ctg acc atg atc	618
Leu Gly Arg Phe Arg Ser Gly Met Leu Arg Trp Val Leu Thr Met Ile	
120 125 130 135	
agc aac tgg ttc ccg gac aag gaa cgc ggg cgc gcc aac gcc atc gtc	666
Ser Asn Trp Phe Pro Asp Lys Glu Arg Gly Arg Ala Asn Ala Ile Val	
140 145 150	
atc atg ttc gtg ccg atc gcc ggc atc ctt acc gca ccg ctg tcc ggc	714
Ile Met Phe Val Pro Ile Ala Gly Ile Leu Thr Ala Pro Leu Ser Gly	
155 160 165	
tgg atc atc acc gcc tgg gac tgg cgc atg ctg ttc ctg gtc gag ggc	762
Trp Ile Ile Thr Ala Trp Asp Trp Arg Met Leu Phe Leu Val Glu Gly	
170 175 180	
gcg ctg tcg ctg gtc gtg atg gtg ctg tgg tat ttc acc atc agc aac	810
Ala Leu Ser Leu Val Val Met Val Leu Trp Tyr Phe Thr Ile Ser Asn	
185 190 195	
cgt cca caa gag gcc aaa agg att tcg cag gcg gaa aaa gat tat ctg	858
Arg Pro Gln Glu Ala Lys Arg Ile Ser Gln Ala Glu Lys Asp Tyr Leu	
200 205 210 215	
atc aaa acg ctg cac gac gaa cag ttg ctg atc aaa ggc aaa acg gtg	906
Ile Lys Thr Leu His Asp Glu Gln Leu Leu Ile Lys Gly Lys Thr Val	
220 225 230	
cgc aac gcc tcg ctg cgt cgg gtg ctg ggc gac aaa atc atg tgg aag	954
Arg Asn Ala Ser Leu Arg Arg Val Leu Gly Asp Lys Ile Met Trp Lys	
235 240 245	
ttc ttc tac cag acc ggg ata tac ggc tac acc ctg tgg ctg ccg acc	1002
Phe Phe Tyr Gln Thr Gly Ile Tyr Gly Tyr Thr Leu Trp Leu Pro Thr	
250 255 260	
att ctc aag ggg ctc acc aac ggc aat atg gag cag gtc ggg atg ctg	1050
Ile Leu Lys Gly Leu Thr Asn Gly Asn Met Glu Gln Val Gly Met Leu	
265 270 275	
gct atc ctg ccc tat atc ggc gcc atc ttc ggc atg ctg atc att tcc	1098
Ala Ile Leu Pro Tyr Ile Gly Ala Ile Phe Gly Met Leu Ile Ile Ser	
280 285 290 295	
acc ctc tcc gat cgc acc ggc aag cgc aaa gtg ttc gtc gca ctg ccg	1146
Thr Leu Ser Asp Arg Thr Gly Lys Arg Lys Val Phe Val Ala Leu Pro	
300 305 310	
ctg gcc tgc ttt gcc atc tgc atg gcg ctg tcg gtg ctg ctg aag gat	1194
Leu Ala Cys Phe Ala Ile Cys Met Ala Leu Ser Val Leu Leu Lys Asp	
315 320 325	
cac atc tgg tgg tcg tac gcg gcg ctg gtg ggc tgt ggc gtc ttt acc	1242

0922501.080301

His Ile Trp Trp Ser Tyr Ala Ala Leu Val Gly Cys Gly Val Phe Thr
330 335 340

cag gcc gcc gcc ggg gtg ttc tgg acc att ccg gcc aag ctg ttt aac 1290
Gln Ala Ala Ala Gly Val Phe Trp Thr Ile Pro Pro Lys Leu Phe Asn
345 350 355

gcc gaa atg gcc ggc ggc gcg cgc ggc gtg atc aat gca ctg ggc aac 1338
Ala Glu Met Ala Gly Gly Ala Arg Gly Val Ile Asn Ala Leu Gly Asn
360 365 370 375

ctc ggc ggt ttc tgc ggc ccc tat atg gtc ggc gtg ttg atc acc ttg 1386
Leu Gly Gly Phe Cys Gly Pro Tyr Met Val Gly Val Leu Ile Thr Leu
380 385 390

ttc agc aaa gac gtc ggc gtt tac agc ctc gcg gtg tcg ctg gcc tcc 1434
Phe Ser Lys Asp Val Gly Val Tyr Ser Leu Ala Val Ser Leu Ala Ser
395 400 405

gcc tcg gtg ctg gcg ttg atg ctg ccg aac aga tgc gac caa aaa gcg 1482
Ala Ser Val Leu Ala Leu Met Leu Pro Asn Arg Cys Asp Gln Lys Ala
410 415 420

ggg gcc gaa taatggacta ttggctgggg ctggactgcg gcggcacctt 1531
Gly Ala Glu
425

tatcaaagcc ggctgtatg accggaatgg cgcagaactg ggcatagccc gccgtacgct 1591
ggacattgtc gcgccgaac ccggctgggc ggaacgtgac atgcccgcgc tgtggcagac 1651
cgccgccgag gtgatccgcg aattgctggc ccgcaacgac attgccgacg ctgatattca 1711
ggccatcggc atctcggcgc agggtaaagg cgcgtttttg ttagacgagc aaggccaacc 1771
gttg 1775

<210> 4
<211> 426
<212> PRT
<213> Unknown

<220>
<223> environmental source

<400> 4
Met Asn Thr Ala Ser Val Ser Val Thr Gln Ser Gln Ala Ile Pro Lys
1 5 10 15
Leu Arg Trp Leu Arg Ile Val Pro Pro Ile Leu Ile Thr Cys Ile Ile
20 25 30
Ser Tyr Met Asp Arg Val Asn Ile Ala Phe Ala Met Pro Gly Gly Met
35 40 45
Asp Asp Glu Leu Gly Ile Thr Ala Ser Met Ala Gly Leu Ala Gly Gly
50 55 60
Ile Phe Phe Ile Gly Tyr Leu Phe Leu Gln Val Pro Gly Gly Lys Leu
65 70 75 80
Ala Val Tyr Gly Asn Gly Lys Lys Phe Ile Gly Trp Ser Leu Leu Ala

0922501.030301

				85					90				95		
Trp	Ala	Val	Ile	Ser	Val	Leu	Thr	Gly	Leu	Val	Thr	Asn	Gln	Tyr	Gln
			100					105					110		
Leu	Leu	Phe	Leu	Arg	Phe	Ala	Leu	Gly	Arg	Phe	Arg	Ser	Gly	Met	Leu
		115					120					125			
Arg	Trp	Val	Leu	Thr	Met	Ile	Ser	Asn	Trp	Phe	Pro	Asp	Lys	Glu	Arg
		130				135					140				
Gly	Arg	Ala	Asn	Ala	Ile	Val	Ile	Met	Phe	Val	Pro	Ile	Ala	Gly	Ile
145				150					155					160	
Leu	Thr	Ala	Pro	Leu	Ser	Gly	Trp	Ile	Ile	Thr	Ala	Trp	Asp	Trp	Arg
			165					170					175		
Met	Leu	Phe	Leu	Val	Glu	Gly	Ala	Leu	Ser	Leu	Val	Val	Met	Val	Leu
		180					185					190			
Trp	Tyr	Phe	Thr	Ile	Ser	Asn	Arg	Pro	Gln	Glu	Ala	Lys	Arg	Ile	Ser
		195				200						205			
Gln	Ala	Glu	Lys	Asp	Tyr	Leu	Ile	Lys	Thr	Leu	His	Asp	Glu	Gln	Leu
	210				215					220					
Leu	Ile	Lys	Gly	Lys	Thr	Val	Arg	Asn	Ala	Ser	Leu	Arg	Arg	Val	Leu
225				230					235					240	
Gly	Asp	Lys	Ile	Met	Trp	Lys	Phe	Phe	Tyr	Gln	Thr	Gly	Ile	Tyr	Gly
			245					250					255		
Tyr	Thr	Leu	Trp	Leu	Pro	Thr	Ile	Leu	Lys	Gly	Leu	Thr	Asn	Gly	Asn
		260					265					270			
Met	Glu	Gln	Val	Gly	Met	Leu	Ala	Ile	Leu	Pro	Tyr	Ile	Gly	Ala	Ile
	275					280					285				
Phe	Gly	Met	Leu	Ile	Ile	Ser	Thr	Leu	Ser	Asp	Arg	Thr	Gly	Lys	Arg
	290				295					300					
Lys	Val	Phe	Val	Ala	Leu	Pro	Leu	Ala	Cys	Phe	Ala	Ile	Cys	Met	Ala
305				310					315					320	
Leu	Ser	Val	Leu	Leu	Lys	Asp	His	Ile	Trp	Trp	Ser	Tyr	Ala	Ala	Leu
			325					330					335		
Val	Gly	Cys	Gly	Val	Phe	Thr	Gln	Ala	Ala	Gly	Val	Phe	Trp	Thr	
	340					345					350				
Ile	Pro	Pro	Lys	Leu	Phe	Asn	Ala	Glu	Met	Ala	Gly	Gly	Ala	Arg	Gly
	355					360					365				
Val	Ile	Asn	Ala	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Cys	Gly	Pro	Tyr	Met
	370				375					380					
Val	Gly	Val	Leu	Ile	Thr	Leu	Phe	Ser	Lys	Asp	Val	Gly	Val	Tyr	Ser
385				390					395					400	
Leu	Ala	Val	Ser	Leu	Ala	Ser	Ala	Ser	Val	Leu	Ala	Leu	Met	Leu	Pro
			405					410					415		
Asn	Arg	Cys	Asp	Gln	Lys	Ala	Gly	Ala	Glu						
			420				425								

<210> 5
 <211> 1478
 <212> DNA
 <213> Klebsiella oxytoca

<220>
 <221> CDS
 <222> (73) ... (1353)

0922501.080301

<400> 5

ttgcccgcgcg ccgctgctca gaccatcgat cttttctatg atgagcgtca cctcactcac 60
agaggcaaac ct atg aat agt tca acg aat gca aca aaa cgc tgg tgg tac 111

Met Asn Ser Ser Thr Asn Ala Thr Lys Arg Trp Trp Tyr

1

5

10

atc atg cct atc gtg ttt atc acg tat agc ctg gcg tac ctc gac cgc 159

Ile Met Pro Ile Val Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg

15

20

25

gct aac ttc agc ttc gct tcg gcg gcc gga att act gaa gac ctg ggg 207

Ala Asn Phe Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly

30

35

40

45

atc acc aaa ggt atc tcc tcc ctt ctg ggg gcg ctg ttc ttc ctc ggc 255

Ile Thr Lys Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly

50

55

60

tac ttc ttc ttt cag atc ccc ggc gcg att tat gcc gaa cgc cgc agc 303

Tyr Phe Phe Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser

65

70

75

gta cgt aaa ctc att ttc atc tgc ctg atc ctg tgg ggt gcc tgc gcc 351

Val Arg Lys Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala

80

85

90

tca ctc gac cgg gat ggt gca caa tat tcc cgc gct ggg cgg gcg atc 399

Ser Leu Asp Arg Asp Gly Ala Gln Tyr Ser Arg Ala Gly Arg Ala Ile

95

100

105

cgc ttt atc ctt ggc gtg gtc gag gcc gca gtc atg ccg gcg atg ctg 447

Arg Phe Ile Leu Gly Val Val Glu Ala Ala Val Met Pro Ala Met Leu

110

115

120

125

ata tac atc agc aac tgg ttt acc aaa tcc gaa cgc tcg cgc gcc aat 495

Ile Tyr Ile Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn

130

135

140

acc ttc ctg atc ctc ggc aac ccg gtg acg gtg ctg tgg atg tcg gtg 543

Thr Phe Leu Ile Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Val

145

150

155

gtc tcc ggc tac ctg att cag gct ttc ggc tgg cgg gag atg ttt att 591

Val Ser Gly Tyr Leu Ile Gln Ala Phe Gly Trp Arg Glu Met Phe Ile

160

165

170

att gaa ggc gtt ccg gcg gtg att tgg gcc ttc tgc tgg tgg gtg ctg 639

Ile Glu Gly Val Pro Ala Val Ile Trp Ala Phe Cys Trp Trp Val Leu

175

180

185

gta aaa gat aaa ccg tct cag gtc aac tgg ctg gcg gaa agc gaa aag 687

Val Lys Asp Lys Pro Ser Gln Val Asn Trp Leu Ala Glu Ser Glu Lys

09922501.080301

190				195				200				205				
gcc	gca	ttg	cag	gag	cag	ctg	gag	cgc	gaa	cag	cag	ggt	atc	aaa	'ccg	735
Ala	Ala	Leu	Gln	Glu	Gln	Leu	Glu	Arg	Glu	Gln	Gln	Gly	Ile	Lys	Pro	
210				215				220								
gtg	cgc	aac	tac	ggt	gag	gcc	ttc	cgc	tcg	cgt	aac	gtg	gtc	ctg	ctg	783
Val	Arg	Asn	Tyr	Gly	Glu	Ala	Phe	Arg	Ser	Arg	Asn	Val	Val	Leu	Leu	
225				230				235								
tgc	atg	caa	tat	ttc	gcc	tgg	agc	atc	ggg	gtt	tac	ggt	ttc	gtg	ctg	831
Cys	Met	Gln	Tyr	Phe	Ala	Trp	Ser	Ile	Gly	Val	Tyr	Gly	Phe	Val	Leu	
240				245				250								
tgg	ctg	ccg	tca	att	atc	cgc	agc	ggc	ggc	gag	aat	atg	ggc	atg	gtc	879
Trp	Leu	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Gly	Glu	Asn	Met	Gly	Met	Val	
255				260				265								
gag	gtc	ggc	tgg	ctc	tca	tcc	gtc	ccc	tac	ctg	gcg	gca	acc	atc	gcc	927
Glu	Val	Gly	Trp	Leu	Ser	Ser	Val	Pro	Tyr	Leu	Ala	Ala	Thr	Ile	Ala	
270				275				280				285				
atg	atc	gtg	gtc	tcc	tgg	gcc	tcc	gat	aaa	atg	cag	aac	cgc	aag	cta	975
Met	Ile	Val	Val	Ser	Trp	Ala	Ser	Asp	Lys	Met	Gln	Asn	Arg	Lys	Leu	
290				295				300								
ttc	gtc	tgg	ccg	ctg	ctg	ctg	att	gcc	gcc	ttc	gcg	ttt	att	ggc	tcc	1023
Phe	Val	Trp	Pro	Leu	Leu	Leu	Ile	Ala	Ala	Phe	Ala	Phe	Ile	Gly	Ser	
305				310				315								
tgg	gcc	gtc	ggc	gct	aac	cat	ttc	tgg	gtc	tct	tat	acc	ctg	ctg	gtc	1071
Trp	Ala	Val	Gly	Ala	Asn	His	Phe	Trp	Val	Ser	Tyr	Thr	Leu	Leu	Val	
320				325				330								
att	gcc	ggc	gcg	gcg	atg	tac	gcc	ccc	tac	ggg	ccg	ttc	ttc	gcc	atc	1119
Ile	Ala	Gly	Ala	Ala	Met	Tyr	Ala	Pro	Tyr	Gly	Pro	Phe	Phe	Ala	Ile	
335				340				345								
att	ccc	gag	atg	ctg	ccg	cgt	aac	gtc	gcc	ggg	ggc	gcc	atg	gcg	ctg	1167
Ile	Pro	Glu	Met	Leu	Pro	Arg	Asn	Val	Ala	Gly	Gly	Ala	Met	Ala	Leu	
350				355				360				365				
att	aac	agc	atg	ggc	gcg	ctg	ggt	tca	ttc	ttt	ggc	tca	tgg	ttt	gtc	1215
Ile	Asn	Ser	Met	Gly	Ala	Leu	Gly	Ser	Phe	Phe	Gly	Ser	Trp	Phe	Val	
370				375				380								
ggc	tac	ctg	aac	ggc	acc	acc	ggc	agc	ccg	tca	gcc	tcg	tac	att	ttt	1263
Gly	Tyr	Leu	Asn	Gly	Thr	Thr	Gly	Ser	Pro	Ser	Ala	Ser	Tyr	Ile	Phe	
385				390				395								
atg	gga	gtg	gcg	ctt	ttc	gtc	tcg	gta	tgg	ctt	act	ttg	att	gtt	aag	1311
Met	Gly	Val	Ala	Leu	Phe	Val	Ser	Val	Trp	Leu	Thr	Leu	Ile	Val	Lys	
400				405				410								

cct gct aat aat caa aaa ctt ccg ctc ggc gca cgt cac gcc 1353
Pro Ala Asn Asn Gln Lys Leu Pro Leu Gly Ala Arg His Ala
415 420 425

tgaacatta acgcaacgga gaaccgcatg aagccgtcag tcattctcta caaaacgctt 1413
cccgacgacc tgcaacaagc gtctggaaca acactttacc gtcacgcagg tgaaaaacct 1473
gcgtt 1478

<210> 6
<211> 427
<212> PRT
<213> Klebsiella oxytoca

<400> 6
Met Asn Ser Ser Thr Asn Ala Thr Lys Arg Trp Trp Tyr Ile Met Pro
1 5 10 15
Ile Val Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg Ala Asn Phe
20 25 30
Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly Ile Thr Lys
35 40 45
Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly Tyr Phe Phe
50 55 60
Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser Val Arg Lys
65 70 75 80
Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala Ser Leu Asp
85 90 95
Arg Asp Gly Ala Gln Tyr Ser Arg Ala Gly Arg Ala Ile Arg Phe Ile
100 105 110
Leu Gly Val Val Glu Ala Ala Val Met Pro Ala Met Leu Ile Tyr Ile
115 120 125
Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn Thr Phe Leu
130 135 140
Ile Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Val Val Ser Gly
145 150 155 160
Tyr Leu Ile Gln Ala Phe Gly Trp Arg Glu Met Phe Ile Ile Glu Gly
165 170 175
Val Pro Ala Val Ile Trp Ala Phe Cys Trp Trp Val Leu Val Lys Asp
180 185 190
Lys Pro Ser Gln Val Asn Trp Leu Ala Glu Ser Glu Lys Ala Ala Leu
195 200 205
Gln Glu Gln Leu Glu Arg Glu Gln Gln Gly Ile Lys Pro Val Arg Asn
210 215 220
Tyr Gly Glu Ala Phe Arg Ser Arg Asn Val Val Leu Leu Cys Met Gln
225 230 235 240
Tyr Phe Ala Trp Ser Ile Gly Val Tyr Gly Phe Val Leu Trp Leu Pro
245 250 255
Ser Ile Ile Arg Ser Gly Gly Glu Asn Met Gly Met Val Glu Val Gly
260 265 270
Trp Leu Ser Ser Val Pro Tyr Leu Ala Ala Thr Ile Ala Met Ile Val
275 280 285
Val Ser Trp Ala Ser Asp Lys Met Gln Asn Arg Lys Leu Phe Val Trp
290 295 300

09922501-080301

Pro Leu Leu Leu Ile Ala Ala Phe Ala Phe Ile Gly Ser Trp Ala Val
 305 310 315 320
 Gly Ala Asn His Phe Trp Val Ser Tyr Thr Leu Leu Val Ile Ala Gly
 325 330 335
 Ala Ala Met Tyr Ala Pro Tyr Gly Pro Phe Phe Ala Ile Ile Pro Glu
 340 345 350
 Met Leu Pro Arg Asn Val Ala Gly Gly Ala Met Ala Leu Ile Asn Ser
 355 360 365
 Met Gly Ala Leu Gly Ser Phe Phe Gly Ser Trp Phe Val Gly Tyr Leu
 370 375 380
 Asn Gly Thr Thr Gly Ser Pro Ser Ala Ser Tyr Ile Phe Met Gly Val
 385 390 395 400
 Ala Leu Phe Val Ser Val Trp Leu Thr Leu Ile Val Lys Pro Ala Asn
 405 410 415
 Asn Gln Lys Leu Pro Leu Gly Ala Arg His Ala
 420 425

<210> 7
 <211> 1600
 <212> DNA
 <213> Pantoea citrea

<220>
 <221> CDS
 <222> (214)...(1521)

<400> 7
 tctgagcttt tcccgacctt atccctgtca gatccctgcc tgggtcacga accttgtaac 60
 acactttctt aacatgccct tacgtgaccc tgatcccaca ctgtcagtcg aaaaacacgt 120
 tttatagctc ctgataagca cagttcgag cgcgtaactg caccgcagg gttctgcttt 180
 gogtcaactg acaaaacaga aaggggatat atc atg caa aaa tca cag ccg gga 234
 Met Gln Lys Ser Gln Pro Gly
 1 5

acc cgc tgg ttt cgg att att gtg ccg atc ctg ata gcc tgc atc atg 282
 Thr Arg Trp Phe Arg Ile Ile Val Pro Ile Leu Ile Ala Cys Ile Met
 10 15 20

tcg ttt atg gat cgg gta aat atc agt ttc gca ttg ccg ggc ggt atg 330
 Ser Phe Met Asp Arg Val Asn Ile Ser Phe Ala Leu Pro Gly Gly Met
 25 30 35

gag cag gat ctg ctg atg tcc agc cag atg gcc ggg gta gtt agc ggt 378
 Glu Gln Asp Leu Leu Met Ser Ser Gln Met Ala Gly Val Val Ser Gly
 40 45 50 55

att ttc ttt att ggt tat ctg ttt ttg cag gtt cct ggt ggg cat atc 426
 Ile Phe Phe Ile Gly Tyr Leu Phe Leu Gln Val Pro Gly Gly His Ile
 60 65 70

gca gta cgt ggc agt ggt aaa cgt ttt att gcc tgg tcg ctt gtt gcc 474
 Ala Val Arg Gly Ser Gly Lys Arg Phe Ile Ala Trp Ser Leu Val Ala

09922501.080301

75	80	85	
tgg gcc gtt gtt tct gtc gct acc ggg ttt gtg act cat cag tac cag			522
Trp Ala Val Val Ser Val Ala Thr Gly Phe Val Thr His Gln Tyr Gln			
90	95	100	
ctg ttg att tta cgt ttt gca ctg ggg gtc tct gaa ggt ggg atg ttg			570
Leu Leu Ile Leu Arg Phe Ala Leu Gly Val Ser Glu Gly Gly Met Leu			
105	110	115	
cag gta gtt ctg aca atg gtc agc aac tgg ttt cct gaa aaa gag ctg			618
Pro Val Val Leu Thr Met Val Ser Asn Trp Phe Pro Glu Lys Glu Leu			
120	125	130	135
ggg cgt gct aat gca ttt gtc atg atg ttc gcc ccg ctt ggc gga atg			666
Gly Arg Ala Asn Ala Phe Val Met Met Phe Ala Pro Leu Gly Gly Met			
140	145	150	
att acc gcc cct gtc tcc gga tgg att att gca ctg cta gac tgg cgc			714
Ile Thr Ala Pro Val Ser Gly Trp Ile Ile Ala Leu Leu Asp Trp Arg			
155	160	165	
tgg tta ttt att atc gaa gga tta ctg tcc gta gtg gtt ctg gca gtc			762
Trp Leu Phe Ile Ile Glu Gly Leu Leu Ser Val Val Val Leu Ala Val			
170	175	180	
tgg tgg ctg atg gtc agt gac cgc cct gaa gat gcc cgt tgg ctg ccg			810
Trp Trp Leu Met Val Ser Asp Arg Pro Glu Asp Ala Arg Trp Leu Pro			
185	190	195	
gca gca gaa cgg gaa tat ctg ctg cgc gaa atg gcc cgt gac aag gcc			858
Ala Ala Glu Arg Glu Tyr Leu Leu Arg Glu Met Ala Arg Asp Lys Ala			
200	205	210	215
gag cgg agc aaa ctg cct ccg atc agt cat gct ccc ctg caa gag gtt			906
Glu Arg Ser Lys Leu Pro Pro Ile Ser His Ala Pro Leu Gln Glu Val			
220	225	230	
ttc cat aac ccg ggc ctg atg aag tta gtg att ctg aac ttt ttc tat			954
Phe His Asn Pro Gly Leu Met Lys Leu Val Ile Leu Asn Phe Phe Tyr			
235	240	245	
cag aca ggt gat tac gga tac act ctg tgg ctg ccg act att atc aaa			1002
Gln Thr Gly Asp Tyr Gly Tyr Thr Leu Trp Leu Pro Thr Ile Ile Lys			
250	255	260	
aac ctg acc gga gct agt att ggt aac gtc ggt ttg ctg aca gtg cta			1050
Asn Leu Thr Gly Ala Ser Ile Gly Asn Val Gly Leu Leu Thr Val Leu			
265	270	275	
cct ttt atc gcg acg tta tca ggg att tat gtc gtc tct tac ctg agc			1098
Pro Phe Ile Ala Thr Leu Ser Gly Ile Tyr Val Val Ser Tyr Leu Ser			
280	285	290	295

00000001-00000001

Met	Gln	Lys	Ser	Gln	Pro	Gly	Thr	Arg	Trp	Phe	Arg	Ile	Ile	Val	Pro
1				5					10					15	
Ile	Leu	Ile	Ala	Cys	Ile	Met	Ser	Phe	Met	Asp	Arg	Val	Asn	Ile	Ser
			20					25					30		
Phe	Ala	Leu	Pro	Gly	Gly	Met	Glu	Gln	Asp	Leu	Leu	Met	Ser	Ser	Gln
		35					40					45			
Met	Ala	Gly	Val	Val	Ser	Gly	Ile	Phe	Phe	Ile	Gly	Tyr	Leu	Phe	Leu

50		55		60
Gln Val Pro Gly Gly His Ile Ala Val Arg Gly Ser Gly Lys Arg Phe				
65		70		75
Ile Ala Trp Ser Leu Val Ala Trp Ala Val Val Ser Val Ala Thr Gly				80
	85		90	
Phe Val Thr His Gln Tyr Gln Leu Leu Ile Leu Arg Phe Ala Leu Gly				95
	100		105	
Val Ser Glu Gly Gly Met Leu Pro Val Val Leu Thr Met Val Ser Asn				110
	115		120	
Trp Phe Pro Glu Lys Glu Leu Gly Arg Ala Asn Ala Phe Val Met Met				125
	130		135	
Phe Ala Pro Leu Gly Gly Met Ile Thr Ala Pro Val Ser Gly Trp Ile				140
145		150		155
Ile Ala Leu Leu Asp Trp Arg Trp Leu Phe Ile Ile Glu Gly Leu Leu				160
	165		170	
Ser Val Val Val Leu Ala Val Trp Trp Leu Met Val Ser Asp Arg Pro				175
	180		185	
Glu Asp Ala Arg Trp Leu Pro Ala Ala Glu Arg Glu Tyr Leu Leu Arg				190
	195		200	
Glu Met Ala Arg Asp Lys Ala Glu Arg Ser Lys Leu Pro Pro Ile Ser				205
	210		215	
His Ala Pro Leu Gln Glu Val Phe His Asn Pro Gly Leu Met Lys Leu				220
225		230		235
Val Ile Leu Asn Phe Phe Tyr Gln Thr Gly Asp Tyr Gly Tyr Thr Leu				240
	245		250	
Trp Leu Pro Thr Ile Ile Lys Asn Leu Thr Gly Ala Ser Ile Gly Asn				255
	260		265	
Val Gly Leu Leu Thr Val Leu Pro Phe Ile Ala Thr Leu Ser Gly Ile				270
	275		280	
Tyr Val Val Ser Tyr Leu Ser Asp Lys Thr Gly Lys Arg Arg Gln Trp				285
	290		295	
Val Met Ile Ser Leu Phe Cys Phe Ala Ala Cys Leu Leu Ala Ser Val				300
305		310		315
Leu Leu Arg Glu Phe Val Leu Ala Ala Tyr Leu Ala Leu Val Ala Cys				320
	325		330	
Gly Phe Phe Leu Lys Ala Ala Thr Ser Pro Phe Trp Ser Ile Pro Gly				335
	340		345	
Arg Ile Ala Pro Pro Glu Ala Ala Gly Ser Ala Arg Gly Val Ile Asn				350
	355		360	
Gly Leu Gly Asn Leu Gly Gly Phe Cys Gly Pro Trp Leu Val Gly Leu				365
	370		375	
Met Ile Tyr Leu Tyr Gly Gln Asn Ala Ala Val Val Thr Leu Ala Gly				380
385		390		395
Ser Leu Ile Ile Ala Gly Ile Ile Ala Ala Leu Leu Pro Thr Gln Cys				400
	405		410	
Asp Leu Arg Pro Ala Glu Ala Arg Gln Gln Asn Phe Thr Pro Arg Ile				415
	420		425	
His Asp Ala Lys				430
	435			

<210> 9

<211> 1500

0922501-030301

<212> DNA

<213> Pantoea citrea

<220>

<221> CDS

<222> (154)...(1440)

<400> 9

tcagctcagg cctcggattt cgtaaaccgt catgtcttat ttgtcgacgg cggaatgctg 60
gcctcagtat aaaatacagg ggcagacgga atcagagttt gccctgaaga tatcttactg 120
gttgcccctt cggcacacac aggatgttcc ccc atg aat aca agc aga aaa ctg 174

Met Asn Thr Ser Arg Lys Leu

1

5

ccg gtg aaa cgc tgg tgg tat tta atg ccg gtg att ttt att act tac 222
Pro Val Lys Arg Trp Trp Tyr Leu Met Pro Val Ile Phe Ile Thr Tyr
10 15 20

agc ctg gca tat ctg gat cgg gcc aac tac ggc ttt gct gct gcc tct 270
Ser Leu Ala Tyr Leu Asp Arg Ala Asn Tyr Gly Phe Ala Ala Ala Ser
25 30 35

ggg att gaa gca gat ctt gga att agc cgt ggc acc tcc tct ctg att 318
Gly Ile Glu Ala Asp Leu Gly Ile Ser Arg Gly Thr Ser Ser Leu Ile
40 45 50 55

gga gca ctg ttc ttt ctg gcc tac ttc att ttt cag gtg ccc ggg gca 366
Gly Ala Leu Phe Phe Leu Gly Tyr Phe Ile Phe Gln Val Pro Gly Ala
60 65 70

att tat gca gtg aaa cgc agt gtc cgt aaa ctg gtg ttt acc agc ctg 414
Ile Tyr Ala Val Lys Arg Ser Val Arg Lys Leu Val Phe Thr Ser Leu
75 80 85

ctg ttg tgg gga ttt tgt gcc gct gcg acc gga ctt atc agc aat att 462
Leu Leu Trp Gly Phe Cys Ala Ala Thr Gly Leu Ile Ser Asn Ile
90 95 100

ccg gct ctg atg gtg atc cgc ttt gtt ctg ggt gtt gtt gaa gcc gca 510
Pro Ala Leu Met Val Ile Arg Phe Val Leu Gly Val Val Glu Ala Ala
105 110 115

gtg atg cca gcg atg ctg att tac atc agc aac tgg ttc acc cgt cag 558
Val Met Pro Ala Met Leu Ile Tyr Ile Ser Asn Trp Phe Thr Arg Gln
120 125 130 135

gaa cgt tca cgg gct aat acc ttt ctg gta tta ggt aac ccg gtc acg 606
Glu Arg Ser Arg Ala Asn Thr Phe Leu Val Leu Gly Asn Pro Val Thr
140 145 150

gtg tta tgg atg tct att gtt tcc gga tat ctg atc aat gct ttt ggc 654
Val Leu Trp Met Ser Ile Val Ser Gly Tyr Leu Ile Asn Ala Phe Gly
155 160 165

00022501-030301

tgg cgg gaa atg ttt att ttc gag ggt gtg cct gcc tta atc tgg gcc	702
Trp Arg Glu Met Phe Ile Phe Glu Gly Val Pro Ala Leu Ile Trp Ala	
170 175 180	
atc ttc tgg tgg ttt att gtc cgg gac aaa ccg gag cag gtg agc tgg	750
Ile Phe Trp Trp Phe Ile Val Arg Asp Lys Pro Glu Gln Val Ser Trp	
185 190 195	
ctg aca gaa aca gaa aag cag caa ctg gcc agt gca atg gct gaa gag	798
Leu Thr Glu Thr Glu Lys Gln Gln Leu Ala Ser Ala Met Ala Glu Glu	
200 205 210 215	
cag cag gca ata cca ccg atg cgc aat gtg ccg cag gcc ctg cgt tcc	846
Gln Gln Ala Ile Pro Pro Met Arg Asn Val Pro Gln Ala Leu Arg Ser	
220 225 230	
cgc aat gtg gtg gta ctg tgc ctg tta cac gct ctg tgg agc atc gga	894
Arg Asn Val Val Val Leu Cys Leu Leu His Ala Leu Trp Ser Ile Gly	
235 240 245	
gtg tat ggt ttt atg atg tgg atg cca tcg ata ctg cgt agc gct gca	942
Val Tyr Gly Phe Met Met Trp Met Pro Ser Ile Leu Arg Ser Ala Ala	
250 255 260	
tca atg gac att gtc cgg gta ggc tgg ctg gcc gca gtt ccg tat ctg	990
Ser Met Asp Ile Val Arg Val Gly Trp Leu Ala Ala Val Pro Tyr Leu	
265 270 275	
gcc gcg att att act atg ctg gtg att tca tgg ctg tca gat aaa acc	1038
Ala Ala Ile Ile Thr Met Leu Val Ile Ser Trp Leu Ser Asp Lys Thr	
280 285 290 295	
ggg ctg cgt cgg ctt ttt atc tgg cca tta ttg ctg att gcg tca gtt	1086
Gly Leu Arg Arg Leu Phe Ile Trp Pro Leu Leu Leu Ile Ala Ser Val	
300 305 310	
act ttt ttt ggg tcc tgg tta ctt ggg agc tac tca ttc tgg ttt tcc	1134
Thr Phe Phe Gly Ser Trp Leu Leu Gly Ser Tyr Ser Phe Trp Phe Ser	
315 320 325	
tat ggc ttg ctg gta ctg gct gct gct tgt atg tat gcc ccg tat gga	1182
Tyr Gly Leu Leu Val Leu Ala Ala Ala Cys Met Tyr Ala Pro Tyr Gly	
330 335 340	
ccg ttt ttt gcg ttg att cct gaa ttg ctg cca aaa aat gtg gcg ggg	1230
Pro Phe Phe Ala Leu Ile Pro Glu Leu Leu Pro Lys Asn Val Ala Gly	
345 350 355	
att tct atc ggg tta att aac tgt tgc ggg gcg ctg gga gct ttt gcc	1278
Ile Ser Ile Gly Leu Ile Asn Cys Cys Gly Ala Leu Gly Ala Phe Ala	
360 365 370 375	

0092501.030301

gga gcc tgg ctg gtg ggc tat ctt aat ggt ctg acc ggt ggt ccg ggg 1326
Gly Ala Trp Leu Val Gly Tyr Leu Asn Gly Leu Thr Gly Gly Pro Gly
380 385 390

gct tct tac act ttt atg gcc att gca ttg ctg gtt tct gta ggg ttg 1374
Ala Ser Tyr Thr Phe Met Ala Ile Ala Leu Leu Val Ser Val Gly Leu
395 400 405

gtg ttt ttc ctg aaa gtc cct tca ggg aat ttg gtc act cgt cgg ttg 1422
Val Phe Phe Leu Lys Val Pro Ser Gly Asn Leu Val Thr Arg Arg Leu
410 415 420

ctg aaa ggt gat gca aag taaaaggaat agcgatgaaa cggaacagga 1470
Leu Lys Gly Asp Ala Lys
425

tgtctttgca ggatattgcg gacctcgccg 1500

<210> 10
<211> 429
<212> PRT
<213> Pantoea citrea

<400> 10
Met Asn Thr Ser Arg Lys Leu Pro Val Lys Arg Trp Trp Tyr Leu Met
1 5 10 15
Pro Val Ile Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg Ala Asn
20 25 30
Tyr Gly Phe Ala Ala Ala Ser Gly Ile Glu Ala Asp Leu Gly Ile Ser
35 40 45
Arg Gly Thr Ser Ser Leu Ile Gly Ala Leu Phe Phe Leu Gly Tyr Phe
50 55 60
Ile Phe Gln Val Pro Gly Ala Ile Tyr Ala Val Lys Arg Ser Val Arg
65 70 75 80
Lys Leu Val Phe Thr Ser Leu Leu Leu Trp Gly Phe Cys Ala Ala Ala
85 90 95
Thr Gly Leu Ile Ser Asn Ile Pro Ala Leu Met Val Ile Arg Phe Val
100 105 110
Leu Gly Val Val Glu Ala Ala Val Met Pro Ala Met Leu Ile Tyr Ile
115 120 125
Ser Asn Trp Phe Thr Arg Gln Glu Arg Ser Arg Ala Asn Thr Phe Leu
130 135 140
Val Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Ile Val Ser Gly
145 150 155 160
Tyr Leu Ile Asn Ala Phe Gly Trp Arg Glu Met Phe Ile Phe Glu Gly
165 170 175
Val Pro Ala Leu Ile Trp Ala Ile Phe Trp Trp Phe Ile Val Arg Asp
180 185 190
Lys Pro Glu Gln Val Ser Trp Leu Thr Glu Thr Glu Lys Gln Gln Leu
195 200 205
Ala Ser Ala Met Ala Glu Glu Gln Gln Ala Ile Pro Pro Met Arg Asn
210 215 220
Val Pro Gln Ala Leu Arg Ser Arg Asn Val Val Val Leu Cys Leu Leu

09922501.080301

```
<210> 11
<211> 1500
<212> DNA
<213> Klebsiella oxytoca
```

```
<400> 11
ctaaaacaag cacaataata ataatcacct tcatcaccag aatattttta atattacgag 60
actataaag atg aat ata acc tct aac tct aca acc aaa gat ata ccg cgc 111
```

cag cgc tgg tta aga atc att ccg cct ata ctg atc act tgt att att 159
Gln Arg Trp Leu Arg Ile Ile Pro Pro Ile Leu Ile Thr Cys Ile Ile
15 20 25 30

tct tat atg gac cgg gtc aat att gcc ttt gcg atg ccc gga ggt atg 207
Ser Tyr Met Asp Arg Val Asn Ile Ala Phe Ala Met Pro Gly Gly Met
 35 40 45

gat gcc gac tta ggt att tcc gcc acc atg gcg ggg ctg gcg ggc ggt 255
Asp Ala Asp Leu Gly Ile Ser Ala Thr Met Ala Gly Leu Ala Gly Gly
50 55 60

att	ttc	ttt	atc	ggt	tat	cta	ttt	tta	cag	gtt	ccc	ggc	ggg	aaa	att	303
Ile	Phe	Phe	Ile	Gly	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Gly	Gly	Lys	Ile	
65						70						75				
gcc	gtt	cac	ggt	agc	ggt	aag	aaa	ttt	atc	ggc	tgg	tcg	ctg	gtc	gcc	351
Ala	Val	His	Gly	Ser	Gly	Lys	Lys	Phe	Ile	Gly	Trp	Ser	Leu	Val	Ala	
80						85						90				
tgg	gcg	gtc	atc	tcc	gtg	ctg	acg	ggg	tta	att	acc	aat	cag	tac	cag	399
Trp	Ala	Val	Ile	Ser	Val	Leu	Thr	Gly	Leu	Ile	Thr	Asn	Gln	Tyr	Gln	
95			100						105			110				
ctg	ctg	gcc	ctg	cgc	ttc	tta	ctg	ggc	gtg	gcg	gaa	ggc	ggt	atg	ctg	447
Leu	Leu	Ala	Leu	Arg	Phe	Leu	Leu	Gly	Val	Ala	Glu	Gly	Gly	Met	Leu	
			115						120			125				
ccg	gtc	gtt	ctc	acg	atg	atc	agt	aac	tgg	ttc	ccc	gac	gct	gaa	cgc	495
Pro	Val	Val	Leu	Thr	Met	Ile	Ser	Asn	Trp	Phe	Pro	Asp	Ala	Glu	Arg	
130						135						140				
ggt	cgc	gcc	aac	gcg	att	gtc	att	atg	ttt	gtg	ccg	att	gcc	ggg	att	543
Gly	Arg	Ala	Asn	Ala	Ile	Val	Ile	Met	Phe	Val	Pro	Ile	Ala	Gly	Ile	
145						150						155				
atc	acc	gcc	cca	ctc	tca	ggc	tgg	att	atc	acg	gtt	ctc	gac	tgg	cgc	591
Ile	Thr	Ala	Pro	Leu	Ser	Gly	Trp	Ile	Ile	Thr	Val	Leu	Asp	Trp	Arg	
160						165						170				
tgg	ctg	ttt	att	atc	gaa	ggt	ttg	ctc	tcg	ctg	gtt	gtt	ctg	gtt	ctg	639
Trp	Leu	Phe	Ile	Ile	Glu	Gly	Leu	Leu	Ser	Leu	Val	Val	Leu	Val	Leu	
175			180						185			190				
tgg	gca	tac	acc	atc	tat	gac	cgt	ccg	cag	gaa	gcg	cgc	tgg	att	tcc	687
Trp	Ala	Tyr	Thr	Ile	Tyr	Asp	Arg	Pro	Gln	Glu	Ala	Arg	Trp	Ile	Ser	
			195						200			205				
gaa	gca	gag	aag	cgc	tat	ctg	gtc	gag	acg	ctg	gcc	gcg	gag	caa	aaa	735
Glu	Ala	Glu	Lys	Arg	Tyr	Leu	Val	Glu	Thr	Leu	Ala	Ala	Glu	Gln	Lys	
210						215						220				
gcc	att	gcc	ggc	acc	gag	gtg	aaa	aac	gcc	tct	ctg	agc	gcc	gtt	ctc	783
Ala	Ile	Ala	Gly	Thr	Glu	Val	Lys	Asn	Ala	Ser	Leu	Ser	Ala	Val	Leu	
225						230						235				
tcc	gac	aaa	acc	atg	tgg	cag	ctt	atc	gcc	ctg	aac	ttc	ttc	tac	cag	831
Ser	Asp	Lys	Thr	Met	Trp	Gln	Leu	Ile	Ala	Leu	Asn	Phe	Phe	Tyr	Gln	
240						245						250				
acc	ggc	att	tac	ggc	tac	acc	ctg	tgg	cta	ccc	acc	att	ctg	aaa	gaa	879
Thr	Gly	Ile	Tyr	Gly	Tyr	Thr	Leu	Trp	Leu	Pro	Thr	Ile	Leu	Lys	Glu	
255			260						265			270				

ttg acc cat agc agc atg ggg cag gtc ggc atg ctt gcc att ctg ccg	927
Leu Thr His Ser Ser Met Gly Gln Val Gly Met Leu Ala Ile Leu Pro	
275 280 285	
tac gtc ggc gcc att gct ggg atg ttc ctg ttt tcc tcc ctt tca gac	975
Tyr Val Gly Ala Ile Ala Gly Met Phe Leu Phe Ser Ser Leu Ser Asp	
290 295 300	
cga acc ggt aaa cgc aag ctg ttc gtc tgc ctg ccg ctg att ggc ttc	1023
Arg Thr Gly Lys Arg Lys Leu Phe Val Cys Leu Pro Leu Ile Gly Phe	
305 310 315	
gct ctg tgc atg ttc ctg tgc gtg gcg ctg aaa aac caa att tgg ctc	1071
Ala Leu Cys Met Phe Leu Ser Val Ala Leu Lys Asn Gln Ile Trp Leu	
320 325 330	
tcc tat gcc gcg ctg gtc ggc tgc gga ttc ttc ctg caa tgc gcg gct	1119
Ser Tyr Ala Ala Leu Val Gly Cys Gly Phe Phe Leu Gln Ser Ala Ala	
335 340 345 350	
ggc gtg ttc tgg acc atc ccg gca cgt ctg ttc agc gcg gaa atg gcg	1167
Gly Val Phe Trp Thr Ile Pro Ala Arg Leu Phe Ser Ala Glu Met Ala	
355 360 365	
ggc ggc gcg cgc ggg gtt atc aac gcg ctt ggc aac ctc ggc gga ttt	1215
Gly Gly Ala Arg Gly Val Ile Asn Ala Leu Gly Asn Leu Gly Gly Phe	
370 375 380	
tgt ggc cct tat gcg gtc ggg gtg ctg atc acg ttg tac agc aaa gac	1263
Cys Gly Pro Tyr Ala Val Gly Val Leu Ile Thr Leu Tyr Ser Lys Asp	
385 390 395	
gct ggc gtc tat tgc ctg gcg atc tcc ctg gcg ctg gcc gcg ctg atg	1311
Ala Gly Val Tyr Cys Leu Ala Ile Ser Leu Ala Leu Ala Ala Leu Met	
400 405 410	
gcg ctg ctg ctg ccg gcg aaa tgc gat gcc ggt gct gcg ccg gta aag	1359
Ala Leu Leu Leu Pro Ala Lys Cys Asp Ala Gly Ala Ala Pro Val Lys	
415 420 425 430	
acg ata aat cca cat aaa cgc act gcg taaactcgag cccggcggcg	1406
Thr Ile Asn Pro His Lys Arg Thr Ala	
435	
ctgcgcctgc cgggcctgcg aaatatgccg ggttcacccg gtaacaatga gatgcgaaag	1466
atgagcaaga aacaggcctt ctggctgggt attg	1500

<210> 12

<211> 439

<212> PRT

<213> Klebsiella oxytoca

<400> 12

0992501.080301

Met	Asn	Ile	Thr	Ser	Asn	Ser	Thr	Thr	Lys	Asp	Ile	Pro	Arg	Gln	Arg
1				5					10					15	
Trp	Leu	Arg	Ile	Ile	Pro	Pro	Ile	Leu	Ile	Thr	Cys	Ile	Ile	Ser	Tyr
		20						25					30		
Met	Asp	Arg	Val	Asn	Ile	Ala	Phe	Ala	Met	Pro	Gly	Gly	Met	Asp	Ala
	35					40					45				
Asp	Leu	Gly	Ile	Ser	Ala	Thr	Met	Ala	Gly	Leu	Ala	Gly	Gly	Ile	Phe
	50					55					60				
Phe	Ile	Gly	Tyr	Leu	Phe	Leu	Gln	Val	Pro	Gly	Gly	Lys	Ile	Ala	Val
65					70					75					80
His	Gly	Ser	Gly	Lys	Phe	Ile	Gly	Trp	Ser	Leu	Val	Ala	Trp	Ala	
			85					90					95		
Val	Ile	Ser	Val	Leu	Thr	Gly	Leu	Ile	Thr	Asn	Gln	Tyr	Gln	Leu	Leu
			100					105					110		
Ala	Leu	Arg	Phe	Leu	Leu	Gly	Val	Ala	Glu	Gly	Gly	Met	Leu	Pro	Val
	115					120						125			
Val	Leu	Thr	Met	Ile	Ser	Asn	Trp	Phe	Pro	Asp	Ala	Glu	Arg	Gly	Arg
	130					135					140				
Ala	Asn	Ala	Ile	Val	Ile	Met	Phe	Val	Pro	Ile	Ala	Gly	Ile	Ile	Thr
145					150					155					160
Ala	Pro	Leu	Ser	Gly	Trp	Ile	Ile	Thr	Val	Leu	Asp	Trp	Arg	Trp	Leu
			165					170						175	
Phe	Ile	Ile	Glu	Gly	Leu	Leu	Ser	Leu	Val	Val	Leu	Val	Leu	Trp	Ala
		180						185					190		
Tyr	Thr	Ile	Tyr	Asp	Arg	Pro	Gln	Glu	Ala	Arg	Trp	Ile	Ser	Glu	Ala
	195					200						205			
Glu	Lys	Arg	Tyr	Leu	Val	Glu	Thr	Leu	Ala	Ala	Glu	Gln	Lys	Ala	Ile
	210					215					220				
Ala	Gly	Thr	Glu	Val	Lys	Asn	Ala	Ser	Leu	Ser	Ala	Val	Leu	Ser	Asp
225					230					235					240
Lys	Thr	Met	Trp	Gln	Leu	Ile	Ala	Leu	Asn	Phe	Phe	Tyr	Gln	Thr	Gly
			245					250						255	
Ile	Tyr	Gly	Tyr	Thr	Leu	Trp	Leu	Pro	Thr	Ile	Leu	Lys	Glu	Leu	Thr
		260					265						270		
His	Ser	Ser	Met	Gly	Gln	Val	Gly	Met	Leu	Ala	Ile	Leu	Pro	Tyr	Val
	275						280					285			
Gly	Ala	Ile	Ala	Gly	Met	Phe	Leu	Phe	Ser	Ser	Leu	Ser	Asp	Arg	Thr
	290					295					300				
Gly	Lys	Arg	Lys	Leu	Phe	Val	Cys	Leu	Pro	Leu	Ile	Gly	Phe	Ala	Leu
305					310					315					320
Cys	Met	Phe	Leu	Ser	Val	Ala	Leu	Lys	Asn	Gln	Ile	Trp	Leu	Ser	Tyr
			325					330						335	
Ala	Ala	Leu	Val	Gly	Cys	Gly	Phe	Phe	Leu	Gln	Ser	Ala	Ala	Gly	Val
		340						345					350		
Phe	Trp	Thr	Ile	Pro	Ala	Arg	Leu	Phe	Ser	Ala	Glu	Met	Ala	Gly	Gly
	355						360					365			
Ala	Arg	Gly	Val	Ile	Asn	Ala	Leu	Gly	Asn	Leu	Gly	Gly	Phe	Cys	Gly
	370					375					380				
Pro	Tyr	Ala	Val	Gly	Val	Leu	Ile	Thr	Leu	Tyr	Ser	Lys	Asp	Ala	Gly
385					390					395					400
Val	Tyr	Cys	Leu	Ala	Ile	Ser	Leu	Ala	Leu	Ala	Ala	Leu	Met	Ala	Leu
			405					410						415	
Leu	Leu	Pro	Ala	Lys	Cys	Asp	Ala	Gly	Ala	Ala	Pro	Val	Lys	Thr	Ile

00922501.080301

420
Asn Pro His Lys Arg Thr Ala
435

425

430

<210> 13
<211> 3153
<212> DNA
<213> Unknown

<220>
<223> environmental source

<221> CDS
<222> (292)...(1236)

<221> CDS
<222> (1252)...(2280)

<221> CDS
<222> (2293)...(3045)

<400> 13
catgcctgca ggtcgactct agaggatctc gccgcgcctc aggtcgaggg atacactcgt 60
cagcgctttc gtgccgccga actccttcga aacggcacga aactccagaa gtttgtccgt 120
atccaccccg ctctcccaa agctttatga ggctatagga tattgatatg gtatcgataa 180
cactcctgtc aagaggcggg ttccacgcca ggccgggaggg caaaatagga ctggacaatt 240
ccttcaagcg ggatatgtta tcgataacaa atcatcttcc ggaggagagc c atg agc 297
Met Ser
1

aag atc gat gtg ttg cag gtc ggt ccc tac cct gca tgg gac gag gag 345
Lys Ile Asp Val Leu Gln Val Gly Pro Tyr Pro Ala Trp Asp Glu Glu
5 10 15

cgc ctg aac gcg acc ttc acg atg cac cgc tat ttc gag gcg gcc gac 393
Arg Leu Asn Ala Thr Phe Thr Met His Arg Tyr Phe Glu Ala Ala Asp
20 25 30

aag gcg gcg ttt ctg gcc gag cac ggc ggc acg atc cgc ggc atc gcc 441
Lys Ala Ala Phe Leu Ala Glu His Gly Gly Thr Ile Arg Gly Ile Ala
35 40 45 50

acg cgc ggc gag ctt ggt gcc aac cgg gcg atg atc gag gcg ctg ccg 489
Thr Arg Gly Glu Leu Gly Ala Asn Arg Ala Met Ile Glu Ala Leu Pro
55 60 65

aag ctg gaa gtg atc tcg gtc tac ggc gtc ggc ttc gat gcg gtg gac 537
Lys Leu Glu Val Ile Ser Val Tyr Gly Val Gly Phe Asp Ala Val Asp
70 75 80

ctt tcg gcg gcc cgc gag cgc ggc atc cgc gtc acc aac acg ccc gac 585
Leu Ser Ala Ala Arg Glu Arg Gly Ile Arg Val Thr Asn Thr Pro Asp

0992501-030301

85	90	95	
gtg ctc acc aag gac	gtg gcc gat ctc ggc atc gcc atg atg ctg gcg	633	
Val Leu Thr Lys Asp	Val Ala Asp Leu Gly Ile Ala Met Met Leu Ala		
100	105 110		
cag gcg cgc ggc gtc atc ggc gga gag gcc tgg gtg aag agc ggc gat	681		
Gln Ala Arg Gly Val Ile Gly Gly Glu Ala Trp Val Lys Ser Gly Asp			
115 120 125 130			
tgg gca agc aag ggt ctc tat ccg ctg aag cgc cgc gta cat ggc atg	729		
Trp Ala Ser Lys Gly Leu Tyr Pro Leu Lys Arg Arg Val His Gly Met			
135 140 145			
cgc gcc ggg gtg ctc ggc ctc ggc cgc atc ggc tac gag gtg gcc aag	777		
Arg Ala Gly Val Leu Gly Leu Gly Arg Ile Gly Tyr Glu Val Ala Lys			
150 155 160			
cgc ctt gcc ggc ttc gac atg gac atc gcc tac agc gac acc ggc ccg	825		
Arg Leu Ala Gly Phe Asp Met Asp Ile Ala Tyr Ser Asp Thr Gly Pro			
165 170 175			
aag gat ttc gcc agg gac tgg acc ttc gtc gcc gat ccg gcg gag ctg	873		
Lys Asp Phe Ala Arg Asp Trp Thr Phe Val Ala Asp Pro Ala Glu Leu			
180 185 190			
gcc gcc cgc tcc gac ttc ctc ttc gtc acg ctc gcc gcc tcc gcc gag	921		
Ala Ala Arg Ser Asp Phe Leu Phe Val Thr Leu Ala Ala Ser Ala Glu			
195 200 205 210			
acg cgc cac atc gtc ggc cgc aag gtc atc gag gcg ctc ggc cct gag	969		
Thr Arg His Ile Val Gly Arg Lys Val Ile Glu Ala Leu Gly Pro Glu			
215 220 225			
ggc atg ctg atc aac atc tcg cgc gct tcc aac atc gat gaa agc gcc	1017		
Gly Met Leu Ile Asn Ile Ser Arg Ala Ser Asn Ile Asp Glu Ser Ala			
230 235 240			
ctt ctc gac gcg ctg gag acg aag gcg ctc ggc tcg gcc gcg ctc gac	1065		
Leu Leu Asp Ala Leu Glu Thr Lys Ala Leu Gly Ser Ala Ala Leu Asp			
245 250 255			
gtc ttc gag ggc gag ccg aac ctc aat ccg cgt ttc ctt gcc ctc gac	1113		
Val Phe Glu Gly Glu Pro Asn Leu Asn Pro Arg Phe Leu Ala Leu Asp			
260 265 270			
aac gtc ctc ttg cag ccg cac atg gcc tcc ggc acg atc gag acc cgc	1161		
Asn Val Leu Leu Gln Pro His Met Ala Ser Gly Thr Ile Glu Thr Arg			
275 280 285 290			
aag gcc atg ggc cag ctc gtc ttc gac aac ctg tcg gcc cat ttc gac	1209		
Lys Ala Met Gly Gln Leu Val Phe Asp Asn Leu Ser Ala His Phe Asp			
295 300 305			

0992501 "050301" 10000000

ggc cgg ccg ctg ccg acc ccg gtt ctg taaggagaga ggtcc atg aag gcg	1260
Gly Arg Pro Leu Pro Thr Pro Val Leu Met Lys Ala	
310 315	
atc gtc atc cat cag gcc aag gac ctg cgc gtc gag gac agc gcc gtc	1308
Ile Val Ile His Gln Ala Lys Asp Leu Arg Val Glu Asp Ser Ala Val	
320 325 330	
gag gcg ccc ggc ccc ggc gag gtg gag atc cgc ctt gcc gcc ggc ggc	1356
Glu Ala Pro Gly Pro Gly Glu Val Glu Ile Arg Leu Ala Ala Gly Gly	
335 340 345 350	
atc tgc ggc tcg gac ctg cac tac tac aac cac ggc ggc ttc ggc acg	1404
Ile Cys Gly Ser Asp Leu His Tyr Tyr Asn His Gly Gly Phe Gly Thr	
355 360 365	
gtg cgc ctc aag gag ccg atg atc ctc ggc cat gag gtt tcc gcc cac	1452
Val Arg Leu Lys Glu Pro Met Ile Leu Gly His Glu Val Ser Gly His	
370 375 380	
gtc gcg gcg ctc ggc gaa ggc gtc tcc ggc ctt gcc atc ggc gac ctc	1500
Val Ala Ala Leu Gly Glu Gly Val Ser Gly Leu Ala Ile Gly Asp Leu	
385 390 395	
gtc gcc gtc tcg ccc tcg cgg ccc tgc ggg gcg tgc gac tat tgc ctc	1548
Val Ala Val Ser Pro Ser Arg Pro Cys Gly Ala Cys Asp Tyr Cys Leu	
400 405 410	
aag ggc ttg gcg aac cat tgc ttc aac atg cgc ttc tac ggc tcg gcc	1596
Lys Gly Leu Ala Asn His Cys Phe Asn Met Arg Phe Tyr Gly Ser Ala	
415 420 425 430	
atg ccc ttc ccg cac atc cag ggc gcg ttc cgc gag cgg ctg gtc gcc	1644
Met Pro Phe Pro His Ile Gln Gly Ala Phe Arg Glu Arg Leu Val Ala	
435 440 445	
aag gcc agc cag tgc gtg aag gct gag ggc ctt tcg gca ggt gaa gcc	1692
Lys Ala Ser Gln Cys Val Lys Ala Glu Gly Leu Ser Ala Gly Glu Ala	
450 455 460	
gcg atg gcc gag ccg ctc tcc gtc acg ctt cac gcc acg cgc cgg gcc	1740
Ala Met Ala Glu Pro Leu Ser Val Thr Leu His Ala Thr Arg Arg Ala	
465 470 475	
ggc gaa atg ctg ggc aag cgc gtg ctc gtc acc ggc tgc ggg ccg atc	1788
Gly Glu Met Leu Gly Lys Arg Val Leu Val Thr Gly Cys Gly Pro Ile	
480 485 490	
ggc acc ctg tcg atc ctc gcc gcc cgg cgc gcc ggc gcg gcg gag atc	1836
Gly Thr Leu Ser Ile Leu Ala Ala Arg Arg Ala Gly Ala Ala Glu Ile	
495 500 505 510	

09922201.F0522560

gtc gcc gct gac ctt tcc gag cgt gca ctc ggc ttt gcc cgc gcc gtc	1884
Val Ala Ala Asp Leu Ser Glu Arg Ala Leu Gly Phe Ala Arg Ala Val	
515 520 525	
ggc gcg gac cgc acg gtc aac ctg tcc gaa gac cgc gac ggc ctc gtt	1932
Gly Ala Asp Arg Thr Val Asn Leu Ser Glu Asp Arg Asp Gly Leu Val	
530 535 540	
ccg ttc agc gag aac aag gga tat ttc gat gtc ctc tac gaa tgc tcc	1980
Pro Phe Ser Glu Asn Lys Gly Tyr Phe Asp Val Leu Tyr Glu Cys Ser	
545 550 555	
ggc gcc cag ccg gcg ctg gtt gcc ggc atc cag gcc ttg cgc ccg cgc	2028
Gly Ala Gln Pro Ala Leu Val Ala Gly Ile Gln Ala Leu Arg Pro Arg	
560 565 570	
ggc gtc atc gtc cag ctc ggc ctc ggc ggc gag atg agc ctt ccc atg	2076
Gly Val Ile Val Gln Leu Gly Leu Gly Gly Glu Met Ser Leu Pro Met	
575 580 585 590	
atg gcg atc acc gcc aag gaa ctg gac ctg cgc ggc tcc ttc cgc ttc	2124
Met Ala Ile Thr Ala Lys Glu Leu Asp Leu Arg Gly Ser Phe Arg Phe	
595 600 605	
cat gag gaa ttc gcc gtc gcc gtg aag ctg atg cag ggc ggc ctc atc	2172
His Glu Glu Phe Ala Val Ala Val Lys Leu Met Gln Gly Gly Leu Ile	
610 615 620	
gac gtg aag ccg ctg atc acc cat act ttg ccg ctt gcc gat gcg ctt	2220
Asp Val Lys Pro Leu Ile Thr His Thr Leu Pro Leu Ala Asp Ala Leu	
625 630 635	
cag gcc ttc gag atc gcc tcc gag aag ggc caa tcc atg aag act cag	2268
Gln Ala Phe Glu Ile Ala Ser Asp Lys Gly Gln Ser Met Lys Thr Gln	
640 645 650	
atc gca ttc agt taaggaagag cc atg agc atc cag ctt ttc gac ctc acg	2319
Ile Ala Phe Ser Met Ser Ile Gln Leu Phe Asp Leu Thr	
655 660 665	
ggc aag cgc gcc ctc gtc acc ggc tcc tcc cag ggt atc ggc tat gcg	2367
Gly Lys Arg Ala Leu Val Thr Gly Ser Ser Gln Gly Ile Gly Tyr Ala	
670 675 680	
ctc gcc aag ggc ctt gcc gcc gcc ggc gcg gac atc gtc ctc aac ggc	2415
Leu Ala Lys Gly Leu Ala Ala Ala Gly Ala Asp Ile Val Leu Asn Gly	
685 690 695	
cgc gac gcg gcc aag ctg gcg gcc gcg gcg cag gaa ctc ggc gca aag	2463
Arg Asp Ala Ala Lys Leu Ala Ala Ala Ala Gln Glu Leu Gly Ala Lys	
700 705 710 715	
cac acg ctc gcc ttc gac gcc acc gac cat gcc gcc gtg cgc gcg gcc	2511

00922501.080301

His Thr Leu Ala Phe Asp Ala Thr Asp His Ala Ala Val Arg Ala Ala	
720 725 730	
atc gac gcc ttc gag gcg gag gtc ggc ccc atc gac atc ctc gtc aac	2559
Ile Asp Ala Phe Glu Ala Glu Val Gly Pro Ile Asp Ile Leu Val Asn	
735 740 745	
aat gcc ggc atg cag cac cgc acg ccg ctg gag gat ttc ccc gcc gat	2607
Asn Ala Gly Met Gln His Arg Thr Pro Leu Glu Asp Phe Pro Ala Asp	
750 755 760	
gcc ttc gag cgc atc ctg aag acc aac atc tcg acg gtc ttc aat gtc	2655
Ala Phe Glu Arg Ile Leu Lys Thr Asn Ile Ser Thr Val Phe Asn Val	
765 770 775	
ggc cag gcc gtc gcg cgc cac atg atc gcg cgc ggc gcg ggc aag atc	2703
Gly Gln Ala Val Ala Arg His Met Ile Ala Arg Gly Ala Gly Lys Ile	
780 785 790 795	
atc aac atc gcc agc gtg cag acc gcg ctc gcc cgc ccc ggc atc gcg	2751
Ile Asn Ile Ala Ser Val Gln Thr Ala Leu Ala Arg Pro Gly Ile Ala	
800 805 810	
ccc tat acc gcc acc aag ggc gcc gtc ggc aac ctc acc aag ggc atg	2799
Pro Tyr Thr Ala Thr Lys Gly Ala Val Gly Asn Leu Thr Lys Gly Met	
815 820 825	
gcg acc gac tgg gcg aaa tac ggc ctg caa tgc aac gcc atc gcg ccg	2847
Ala Thr Asp Trp Ala Lys Tyr Gly Leu Gln Cys Asn Ala Ile Ala Pro	
830 835 840	
ggc tat ttc gac acg ccg ctc aat gcc gcg ctg gtc gcc gat ccg gcc	2895
Gly Tyr Phe Asp Thr Pro Leu Asn Ala Ala Leu Val Ala Asp Pro Ala	
845 850 855	
ttt tcc gcc tgg ctg gaa aag cgc acg ccg gcc ggc cgc tgg ggc aag	2943
Phe Ser Ala Trp Leu Glu Lys Arg Thr Pro Ala Gly Arg Trp Gly Lys	
860 865 870 875	
gtg gag gag ctg atc ggc gcc tgc atc ttt ctt tcc tcc gac gct tcc	2991
Val Glu Glu Leu Ile Gly Ala Cys Ile Phe Leu Ser Ser Asp Ala Ser	
880 885 890	
tcc ttc gtg aac gga cac acg ctc tat gtc gac ggc ggc atc acg gcc	3039
Ser Phe Val Asn Gly His Thr Leu Tyr Val Asp Gly Gly Ile Thr Ala	
895 900 905	
tcg ctc tgaggacaac aggcgcacgcg tcctgatggg cgtcgccggc tgcggcaagt	3095
Ser Leu	
ccgccgtcgg cgcggcgctc gccgcgcggc tcggtgcgat ccccggggtac cgagctcg	3153

0992501-030304

<210> 14
 <211> 315
 <212> PRT
 <213> Unknown

<220>
 <223> environmental source

<400> 14

Met	Ser	Lys	Ile	Asp	Val	Leu	Gln	Val	Gly	Pro	Tyr	Pro	Ala	Trp	Asp
1				5					10					15	
Glu	Glu	Arg	Leu	Asn	Ala	Thr	Phe	Thr	Met	His	Arg	Tyr	Phe	Glu	Ala
			20					25					30		
Ala	Asp	Lys	Ala	Ala	Phe	Leu	Ala	Glu	His	Gly	Gly	Thr	Ile	Arg	Gly
		35					40					45			
Ile	Ala	Thr	Arg	Gly	Glu	Leu	Gly	Ala	Asn	Arg	Ala	Met	Ile	Glu	Ala
	50					55					60				
Leu	Pro	Lys	Leu	Glu	Val	Ile	Ser	Val	Tyr	Gly	Val	Gly	Phe	Asp	Ala
65					70					75				80	
Val	Asp	Leu	Ser	Ala	Ala	Arg	Glu	Arg	Gly	Ile	Arg	Val	Thr	Asn	Thr
				85					90					95	
Pro	Asp	Val	Leu	Thr	Lys	Asp	Val	Ala	Asp	Leu	Gly	Ile	Ala	Met	Met
			100					105					110		
Leu	Ala	Gln	Ala	Arg	Gly	Val	Ile	Gly	Gly	Glu	Ala	Trp	Val	Lys	Ser
		115					120					125			
Gly	Asp	Trp	Ala	Ser	Lys	Gly	Leu	Tyr	Pro	Leu	Lys	Arg	Arg	Val	His
	130					135					140				
Gly	Met	Arg	Ala	Gly	Val	Leu	Gly	Leu	Gly	Arg	Ile	Gly	Tyr	Glu	Val
145					150					155				160	
Ala	Lys	Arg	Leu	Ala	Gly	Phe	Asp	Met	Asp	Ile	Ala	Tyr	Ser	Asp	Thr
				165					170					175	
Gly	Pro	Lys	Asp	Phe	Ala	Arg	Asp	Trp	Thr	Phe	Val	Ala	Asp	Pro	Ala
			180					185					190		
Glu	Leu	Ala	Ala	Arg	Ser	Asp	Phe	Leu	Phe	Val	Thr	Leu	Ala	Ala	Ser
	195						200					205			
Ala	Glu	Thr	Arg	His	Ile	Val	Gly	Arg	Lys	Val	Ile	Glu	Ala	Leu	Gly
	210					215					220				
Pro	Glu	Gly	Met	Leu	Ile	Asn	Ile	Ser	Arg	Ala	Ser	Asn	Ile	Asp	Glu
225					230					235				240	
Ser	Ala	Leu	Leu	Asp	Ala	Leu	Glu	Thr	Lys	Ala	Leu	Gly	Ser	Ala	Ala
				245					250					255	
Leu	Asp	Val	Phe	Glu	Gly	Glu	Pro	Asn	Leu	Asn	Pro	Arg	Phe	Leu	Ala
			260					265					270		
Leu	Asp	Asn	Val	Leu	Leu	Gln	Pro	His	Met	Ala	Ser	Gly	Thr	Ile	Glu
	275						280					285			
Thr	Arg	Lys	Ala	Met	Gly	Gln	Leu	Val	Phe	Asp	Asn	Leu	Ser	Ala	His
	290					295					300				
Phe	Asp	Gly	Arg	Pro	Leu	Pro	Thr	Pro	Val	Leu					
305					310					315					

<210> 15
 <211> 343

00922501.000301

<212> PRT
<213> Unknown

<220>
<223> environmental source

<400> 15

Met	Lys	Ala	Ile	Val	Ile	His	Gln	Ala	Lys	Asp	Leu	Arg	Val	Glu	Asp
1				5					10					15	
Ser	Ala	Val	Glu	Ala	Pro	Gly	Pro	Gly	Glu	Val	Glu	Ile	Arg	Leu	Ala
		20						25					30		
Ala	Gly	Gly	Ile	Cys	Gly	Ser	Asp	Leu	His	Tyr	Tyr	Asn	His	Gly	Gly
	35						40					45			
Phe	Gly	Thr	Val	Arg	Leu	Lys	Glu	Pro	Met	Ile	Leu	Gly	His	Glu	Val
	50					55					60				
Ser	Gly	His	Val	Ala	Ala	Leu	Gly	Glu	Gly	Val	Ser	Gly	Leu	Ala	Ile
65				70						75					80
Gly	Asp	Leu	Val	Ala	Val	Ser	Pro	Ser	Arg	Pro	Cys	Gly	Ala	Cys	Asp
			85						90					95	
Tyr	Cys	Leu	Lys	Gly	Leu	Ala	Asn	His	Cys	Phe	Asn	Met	Arg	Phe	Tyr
		100					105						110		
Gly	Ser	Ala	Met	Pro	Phe	Pro	His	Ile	Gln	Gly	Ala	Phe	Arg	Glu	Arg
	115						120					125			
Leu	Val	Ala	Lys	Ala	Ser	Gln	Cys	Val	Lys	Ala	Glu	Gly	Leu	Ser	Ala
	130					135					140				
Gly	Glu	Ala	Ala	Met	Ala	Glu	Pro	Leu	Ser	Val	Thr	Leu	His	Ala	Thr
145				150						155					160
Arg	Arg	Ala	Gly	Glu	Met	Leu	Gly	Lys	Arg	Val	Leu	Val	Thr	Gly	Cys
			165						170					175	
Gly	Pro	Ile	Gly	Thr	Leu	Ser	Ile	Leu	Ala	Ala	Arg	Arg	Ala	Gly	Ala
		180					185						190		
Ala	Glu	Ile	Val	Ala	Ala	Asp	Leu	Ser	Glu	Arg	Ala	Leu	Gly	Phe	Ala
	195						200					205			
Arg	Ala	Val	Gly	Ala	Asp	Arg	Thr	Val	Asn	Leu	Ser	Glu	Asp	Arg	Asp
	210					215					220				
Gly	Leu	Val	Pro	Phe	Ser	Glu	Asn	Lys	Gly	Tyr	Phe	Asp	Val	Leu	Tyr
225				230						235					240
Glu	Cys	Ser	Gly	Ala	Gln	Pro	Ala	Leu	Val	Ala	Gly	Ile	Gln	Ala	Leu
			245						250					255	
Arg	Pro	Arg	Gly	Val	Ile	Val	Gln	Leu	Gly	Leu	Gly	Gly	Glu	Met	Ser
		260					265						270		
Leu	Pro	Met	Met	Ala	Ile	Thr	Ala	Lys	Glu	Leu	Asp	Leu	Arg	Gly	Ser
	275						280					285			
Phe	Arg	Phe	His	Glu	Glu	Phe	Ala	Val	Ala	Val	Lys	Leu	Met	Gln	Gly
	290					295					300				
Gly	Leu	Ile	Asp	Val	Lys	Pro	Leu	Ile	Thr	His	Thr	Leu	Pro	Leu	Ala
305				310						315					320
Asp	Ala	Leu	Gln	Ala	Phe	Glu	Ile	Ala	Ser	Asp	Lys	Gly	Gln	Ser	Met
			325						330					335	
Lys	Thr	Gln	Ile	Ala	Phe	Ser									
			340												

10E080" T0522660

<220>
<223> environmental source

```
<210> 17
<211> 32
<212> DNA
<213> Artificial Sequence
```

<220>
<223> synthetic construct

```
<400> 17
acccaagctt caccaaaaga gtgaagagga ag
```

<210> 18
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 18
cgtatctaga aaaatattct ggtgatgaag gtga

34

<210> 19
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 19
agactctaga tccacataaa cgcactgcgt aaac

34

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 20
gaggggatcc tggcttcgtg aacgatatac tgg

33

<210> 21
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

<400> 21
aataggatcc ttcacacca gaatattttt a

31

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

0992501.080301

<400> 22

cataggtacc ggctttcaga taggtgcc

28

0922501 080301
T0E080 T0522660